

SEQUENCE LISTING

<110> Liang, Yanbin  
Woodward, David F.

<120> Human Prostaglandin FP Receptor Variants  
and Methods of Using Same

<130> 66872-032

<160> 40

<170> FastSEQ for Windows Version 4.0

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<212> DNA  
<213> Homo sapeins

<220>  
<221> CDS  
<222> (1)...(894)

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Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe  
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tca gta atc ttc atg aca gtg gga atc ttg tca aac agc ctt gcc atc 144  
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45

gcc att ctc atg aag gca tat cag aga ttt aga cag aag tcc aag gca 192  
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60

tcg ttt ctg ctt ttg gcc agc ggc ctg gta atc act gat ttc ttt ggc 240  
Ser Phe Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80

cat ctc atc aat gga gcc ata gca gta ttt gta tat gct tct gat aaa 288  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95

gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt 336  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110

atc tgc atg gtc ttt tct ggt ctg tgc cca ctt ctt cta ggc agt gtc Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val 115 120 125	384
atg gcc att gag cggttgtattggagtcacaaaa ccaata tttcat tct Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser 130 135 140	432
acg aaa att aca tcc aaa cat gtg aaa atg atg tta agt ggt gtg tgc Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys 145 150 155 160	480
ttg ttt gct gtt ttc ata gct ttg ctg ccc atc ctt gga cat cga gac Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp 165 170 175	528
tat aaa att cag gcg tcg agg acc tgg tgg ttc tac aac aca gaa gac Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp 180 185 190	576
atc aaa gac tgg gaa gat aga ttt tat ctt cta ctt ttt tct ttt ctg Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu 195 200 205	624
ggg ctc tta gcc ctt ggt gtt tca ttg ttg tgc aat gca atc aca gga Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly 210 215 220	672
att aca ctt tta aga gtt aaa ttt aaa agt cag cag cac aga caa ggc Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly 225 230 235 240	720
aga tct cat cat ttg gaa atg gta atc cag ctc ctg gcg ata atg tgg Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys 245 250 255	768
gtc tcc tgt att tgg agc cca ttt ctg gga tac aga ata att ttg Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Gly Tyr Arg Ile Ile Leu 260 265 270	816
aat ggg aaa gag aaa tat aaa gta tat gaa gag caa agt gat ttc tta Asn Gly Lys Glu Lys Tyr Lys Val Tyr Glu Glu Gln Ser Asp Phe Leu 275 280 285	864
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290 295	
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Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45  
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60  
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val  
115 120 125  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140  
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
145 150 155 160  
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp  
165 170 175  
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp  
180 185 190  
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu  
195 200 205  
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly  
210 215 220  
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
225 230 235 240  
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys  
245 250 255  
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Gly Tyr Arg Ile Ile Leu  
260 265 270  
Asn Gly Lys Glu Lys Tyr Lys Val Tyr Glu Glu Gln Ser Asp Phe Leu  
275 280 285  
His Arg Leu Gln Trp Pro Thr Leu Glu  
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ctt tca aac aca acc tgc cag acg gaa aac cgg ctt tcc gta ttt ttt 96  
Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe  
20 25 30

tca gta atc ttc atg aca gtg gga atc ttg tca aac agc ctt gcc atc 144  
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45

gcc att ctc atg aag gca tat cag aga ttt aga cag aag tcc aag gca 192  
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60

tcg ttt ctg ctt ttg gcc agc ggc ctg gta atc act gat ttc ttt ggc 240  
Ser Phe Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80

cat ctc atc aat gga gcc ata gca gta ttt gta tat gct tct gat aaa 288  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95

gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt 336  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110

atc tgc atg gtg ttt tct ggt ctg tgc cca ctt ctt cta ggc agt gtg 384  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val  
115 120 125

atg gcc att gag cgg tgt att gga gtc aca aaa cca ata ttt cat tct 432  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140

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Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
145 150 155 160

ttg ttt gct gtt ttc ata gct ttg ctg ccc atc ctt gga cat cga gac 528  
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp  
165 170 175

tat aaa att cag gcg tcg agg acc tgg tgt ttc tac aac aca gaa gac 576  
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp  
180 185 190

atc aaa gac tgg gaa gat aga ttt tat ctt cta ctt ttt tct ttg 624

Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu  
195 200 205

ggg ctc tta gcc ctt ggt gtt tca ttg ttg tgc aat gca atc aca gga 672  
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly  
210 215 220

att aca ctt tta aga gtt aaa ttt aaa agt cag cag cac aga caa ggc 720  
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
225 230 235 240

aga tct cat cat ttg gaa atg gta atc cag ctc ctg gcg ata atg tgt 768  
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys  
245 250 255

gtc tcc tgt att tgt tgg agc cca ttt ctg aaa ata gaa gga aaa ata 816  
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Lys Ile Glu Gly Lys Ile  
260 265 270

aaa gtc aca tga gtgaaggaga aacagaacgc aagggtgaaa acaaggcaat 868  
Lys Val Thr \*  
275

tagggcagca gaaagctgg ggtatgaggg tgaagagagg cactctcatg ttttggaaac 928  
tctgttggaa aggttacaat ggcacacatt ggaataatg gaaatcatc tctggaaacc 988  
tgtgaaacaa cacttttgc tctccgaatg gcaacatgga atcaaatctt agatccttgg 1048  
gtatatattc ttctacgaaa ggctgtcctt aagaatctct ataagcttgc cagtcaatgc 1108  
tgtggagtgc atgtcatcag cttacatatt tggagctta gttccattaa aaattcctta 1168  
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<212> PRT  
<213> Homo sapiens

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Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45  
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60  
Ser Phe Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val  
115 120 125  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser

130	135	140
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys		
145	150	155
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp		160
165	170	175
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp		
180	185	190
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu		
195	200	205
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly		
210	215	220
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly		
225	230	235
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys		240
245	250	255
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260	265	270
Lys Val Thr		
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<222> (1) ... (876)

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ctt tca aac aca acc tgc cag acg gaa aac cgg ctt tcc gta ttt ttt			96
Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe			
20	25	30	
tca gta atc ttc atg aca gtg gga atc ttg tca aac agc ctt gcc atc			144
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile			
35	40	45	
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Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala			
50	55	60	
tcg ttt ctg ctt ttg gcc agc ggc ctg gta atc act gat ttc ttt ggc			240
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly			
65	70	75	80
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His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys			

85	90	95	
gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly 100	105	110	336
atc tgc atg gtg ttt tct ggt ctg tgc cca ctt ctt cta ggc agt gtg Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val 115	120	125	384
atg gcc att gag cgg tgt att gga gtc aca aaa cca ata ttt cat tct Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser 130	135	140	432
acg aaa att aca tcc aaa cat gtg aaa atg atg tta agt ggt gtg tgc Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys 145	150	155	480
ttg ttt gct gtt ttc ata gct ttg ctg ccc atc ctt gga cat cga gac Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp 165	170	175	528
tat aaa att cag gcg tcg agg acc tgg tgt ttc tac aac aca gaa gac Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp 180	185	190	576
atc aaa gac tgg gaa gat aga ttt tat ctt cta ctt ttt tct ttg Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu 195	200	205	624
ggg ctc tta gcc ctt ggt gtt tca ttg ttg tgc aat gca atc aca gga Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly 210	215	220	672
att aca ctt tta aga gtt aaa ttt aaa agt cag cag cac aga caa ggc Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly 225	230	235	720
aga tct cat cat ttg gaa atg gta atc cag ctc ctg gcg ata atg tgt Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys 245	250	255	768
gtc tcc tgt att tgt tgg agc cca ttt ctg gga tac aga ata att ttg Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Gly Tyr Arg Ile Ile Leu 260	265	270	816
aat ggg aaa gag aaa tat aaa gta tat gaa gag caa agt gat ttc tta Asn Gly Lys Glu Lys Tyr Lys Val Tyr Glu Glu Gln Ser Asp Phe Leu 275	280	285	864
cat aga aaa tag aaggaaaaat aaaagtcaca tgagtgaagg agaaaacagaa His Arg Lys *			916
290			

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atggaaatca ttctctggaa acctgtgaaa caacacttt tgctctccga atggcaacat 1096  
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Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45  
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60  
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val  
115 120 125  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140  
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
145 150 155 160  
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp  
165 170 175  
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp  
180 185 190  
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu  
195 200 205  
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly  
210 215 220  
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
225 230 235 240  
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys  
245 250 255  
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Gly Tyr Arg Ile Ile Leu  
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275 280 285  
His Arg Lys  
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<222> (1)...(891)

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ctt tca aac aca acc tgc cag acg gaa aac cgg ctt tcc gta ttt ttt 96  
Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe  
20 25 30  
  
tca gta atc ttc atg aca gtg gga atc ttg tca aac agc ctt gcc atc 144  
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45  
  
gcc att ctc atg aag gca tat cag aga ttt aga cag aag tcc aag gca 192  
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60  
  
tcg ttt ctg ctt ttg gcc agc ggc ctg gta atc act gat ttc ttt ggc 240  
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80  
  
cat ctc atc aat gga gcc ata gca gta ttt gta tat gct tct gat aaa 288  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95  
  
gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt 336  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110  
  
atc tgc atg gtg ttt tct ggt ctg tgc cca ctt ctt cta ggc agt gtg 384  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val  
115 120 125  
  
atg gcc att gag cgg tgt att gga gtc aca aaa cca ata ttt cat tct 432  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140  
  
acg aaa att aca tcc aaa cat gtg aaa atg atg tta agt ggt gtg tgc 480  
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
145 150 155 160  
  
ttg ttt gct gtt ttc ata gct ttg ctg ccc atc ctt gga cat cga gac 528

Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp  
165 170 175

576  
tat aaa att cag gcg tcg agg acc tgg tgt ttc tac aac aca gaa gac  
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp  
180 185 190

624  
atc aaa gac tgg gaa gat aga ttt tat ctt cta ctt ttt tct ttt ctg  
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Phe Ser Phe Leu  
195 200 205

672  
ggg ctc tta gcc ctt ggt gtt tca ttg tgc aat gca atc aca gga  
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly  
210 215 220

720  
att aca ctt tta aga gtt aaa ttt aaa agt cag cag cac aga caa ggc  
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
225 230 235 240

768  
aga tct cat cat ttg gaa atg gta atc cag ctc ctg gcg ata atg tgt  
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys  
245 250 255

816  
gtc tcc tgt att tgt tgg agc cca ttt ctg gtg aaa gaa act cat ctc  
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Val Lys Glu Thr His Leu  
260 265 270

864  
cag atg aga ctt tgg act tgg gac ttt cga gtt aat gct ttg gag gac  
Gln Met Arg Leu Trp Thr Trp Asp Phe Arg Val Asn Ala Leu Glu Asp  
275 280 285

911  
tat tgc gaa ggc ttg act gta ttt tga aatgttacaa tggccaaacat  
Tyr Cys Glu Gly Leu Thr Val Phe \*  
290 295

tggaataaat ggaaatcatt ctctggaaac ctgtgaaaca acacttttg ctctccgaat 971  
ggcaacatgg aatcaaatct tagatccttg ggtatatatt cttctacgaa aggctgtcct 1031  
taagaatctc tataagcttg ccagtcaatg ctgtggagtg catgtcatca gcttacatat 1091  
ttgggagctt agttccatta aaaattcctt aaagggttgct gctatttctg agtcaccagt 1151  
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<210> 8  
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Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45

Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60  
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val  
115 120 125  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140  
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
145 150 155 160  
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp  
165 170 175  
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp  
180 185 190  
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu  
195 200 205  
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly  
210 215 220  
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
225 230 235 240  
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys  
245 250 255  
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Val Lys Glu Thr His Leu  
260 265 270  
Gln Met Arg Leu Trp Thr Trp Asp Phe Arg Val Asn Ala Leu Glu Asp  
275 280 285  
Tyr Cys Glu Gly Leu Thr Val Phe  
290 295

<210> 9  
<211> 1221  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)...(804)

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Met Ser Met Asn Asn Ser Lys Gln Leu Val Ser Pro Ala Ala Leu  
1 5 10 15  
ctt tca aac aca acc tgc cag acg gaa aac cgg ctt tcc gta ttt ttt 96  
Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe  
20 25 30  
tca gta atc ttc atg aca gtg gga atc ttg tca aac agc ctt gcc atc 144

Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile				
35	40	45		
gcc att ctc atg aag gca tat cag aga ttt aga cag aag tcc aag gca				192
Ala Ile Leu Met Lys Ala Tyr Gin Arg Phe Arg Gln Lys Ser Lys Ala				
50	55	60		
tcg ttt ctg ctt ttg gcc agc ggc ctg gta atc act gat ttc ttt ggc				240
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly				
65	70	75	80	
cat ctc atc aat gga gcc ata gca gta ttt gta tat gct tct gat aaa				288
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys				
85	90	95		
gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt				336
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly				
100	105	110		
atc tgc atg gtg ttt tct ggt ctg tgc cca ctt ctt cta ggc agt gtg				384
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val				
115	120	125		
atg gcc att gag cgg tgt att gga gtc aca aaa cca ata ttt cat tct				432
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser				
130	135	140		
acg aaa att aca tcc aaa cat gtg aaa atg atg tta agt ggt gtg tgc				480
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys				
145	150	155	160	
ttg ttt gct gtt ttc ata gct ttg ctg ccc atc ctt gga cat cga gac				528
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp				
165	170	175		
tat aaa att cag gcg tcg agg acc tgg tgt ttc tac aac aca gaa gac				576
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp				
180	185	190		
atc aaa gac tgg gaa gat aga ttt tat ctt cta ctt ttt tct ttg ctg				624
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Phe Ser Phe Leu				
195	200	205		
ggg ctc tta gcc ctt ggt gtt tca ttg ttg tgc aat gca atc aca gga				672
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly				
210	215	220		
att aca ctt tta aga gtt aaa ttt aaa agt cag cag cac aga caa ggc				720
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly				
225	230	235	240	
aga tct cat cat ttg gaa atg gta atc cag ctc ctg gcg ata atg tgt				768
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys				

245

250

255

gtc tcc tgt att tgt tgg agc cca ttt ctg cga taa gacactcaac 814  
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Arg \*  
260 265

gagaaaatgac agaaaaacaa ggtgtggatg gagaggcaac atgaaaagtgg atcaaacaac 874  
ttatacatgg gtgctggctc agacgtgaca cctgaggctc cagaactgga agtttatgcc 934  
gtcaagttac aatggccaac attggaataa atggaaatca ttctctggaa acctgtgaaa 994  
caacacttt tgctctccga atggcaacat ggaatcaa attagatcct tgggtatata 1054  
ttcttctacg aaaggctgtc cttagaatac tctataagct tgccagtcaa tgctgtggag 1114  
tgcatgtcat cagcttacat atttgggagc tttagttccat taaaaattcc ttaaaggttg 1174  
ctgctatttc tgagtcacca gttcagaga aatcagcaag cacctag 1221

<210> 10

<211> 267

<212> PRT

<213> Homo sapiens

<400> 10

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1 5 10 15  
Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe  
20 25 30  
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45  
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60  
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val  
115 120 125  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140  
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
145 150 155 160  
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp  
165 170 175  
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp  
180 185 190  
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu  
195 200 205  
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly  
210 215 220  
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
225 230 235 240  
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys  
245 250 255  
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Arg

260

265

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<210> 11
<211> 1328
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) ... (825)

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Met Ser Met Asn Asn Ser Lys Gln Leu Val Ser Pro Ala Ala Ala Leu  
1 5 10 15

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ctt tca aac aca acc tgc cag acg gaa aac cgg ctt tcc gta ttt ttt      96
Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe
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tca gta atc ttc atg aca gtg gga atc ttg tca aac agc ctt gcc atc 144  
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45

gcc att ctc atg aag gca tat cag aga ttt aga cag aag tcc aag gca 192  
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60

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tcg ttt ctg ctt ttg gcc agc ggc ctg gta atc act act gat ttc ttt ggc 240
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly
  65           70           75           80

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cat ctc atc aat gga gcc ata gca gta ttt gta tat gct tct gat aaa	288	
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys		
85	90	95

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gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt 336
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly
          100          105          110

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atc tgc atg gtg ttt tct ggt ctg tgc cca ctt ctt cta ggc agt gtg 384
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val
           115           120           125

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atg gcc att gag cgg tgt att gga gtc aca aaa cca ata ttt cat tct 432  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140

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acg aaa att aca tcc aaa cat gtg aaa atg atg tta agt ggt gtg tgc 480
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys
145           150           155           160

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ttg ttt gct gtt ttc ata gct ttg ctg ccc atc ctt gga cat cga gac	528	
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp		
165	170	175
tat aaa att cag gcg tcg agg acc tgg tgt ttc tac aac aca gaa gac	576	
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp		
180	185	190
atc aaa gac tgg gaa gat aga ttt tat ctt cta ctt ttt tct ttt ctg	624	
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu		
195	200	205
ggg ctc tta gcc ctt ggt gtt tca ttg tgc aat gca atc aca gga	672	
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly		
210	215	220
att aca ctt tta aga gtt aaa ttt aaa agt cag cag cac aga caa ggc	720	
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly		
225	230	235
aga tct cat cat ttg gaa atg gta atc cag ctc ctg gcg ata atg tgt	768	
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys		
245	250	255
gtc tcc tgt att tgt tgg agc cca ttt ctg aca cat tgg ggt aaa gaa	816	
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Thr His Trp Gly Lys Glu		
260	265	270
att cca tga tccctcctgt gcctaagcca ccccagtgga cctggcttc	865	
Ile Pro *		

ttgcaccatc cctgtggctg gaggttttag atactgacag cgataagaca ctcaacgaga 925  
aatgacagaaa aaacaaggtg tggatggaga ggcaacatga aagtggatca aacaacttat 985  
acatgggtgc tggctcagac gtgacacctg aggctccaga actggaagtt tatgccgtca 1045  
agttacaatg gccaacattt gaataaatgg aaatcattct ctggaaacct gtgaaaacaac 1105  
acttttgct ctccgaatgg caacatggaa tcaaatttta gatccttggg tatatattct 1165  
tctacaaag gctgtcctta agaatctcta taagcttgcc agtcaatgct gtggagtgc 1225  
tgtcatcagc ttacatattt gggagcttag ttccattaaa aattccttaa aggttgctgc 1285  
tatttcttag tcaccagttt cagagaaaatc agcaagcacc tag 1328

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<212> PRT  
<213> Homo sapiens

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1 5 10 15  
Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe  
20 25 30  
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45

Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60  
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Gly Ser Val  
115 120 125  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140  
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
145 150 155 160  
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp  
165 170 175  
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp  
180 185 190  
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu  
195 200 205  
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly  
210 215 220  
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
225 230 235 240  
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys  
245 250 255  
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Thr His Trp Gly Lys Glu  
260 265 270  
Ile Pro

<210> 13  
<211> 3095  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (152)...(1228)

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acttgagtgg ttggctttta tctccacaac a atg tcc atg aac aat tcc aaa 172  
Met Ser Met Asn Asn Ser Lys  
1 5

cag cta gtg tct cct gca gct gcg ctt tca aac aca acc tgc cag 220  
Gln Leu Val Ser Pro Ala Ala Leu Leu Ser Asn Thr Thr Cys Gln  
10 15 20

acg gaa aac cgg ctt tcc gta ttt ttc gta atc ttc atg aca gtg 268

Thr Glu Asn Arg Leu Ser Val Phe Phe Ser Val Ile Phe Met Thr Val  
25 30 35

gga atc ttg tca aac agc ctt gcc atc gcc att ctc atg aag gca tat 316  
Gly Ile Leu Ser Asn Ser Leu Ala Ile Ala Ile Leu Met Lys Ala Tyr  
40 45 50 55

cag aga ttt aga cag aag tcc aag gca tcg ttt ctg ctt ttg gcc agc 364  
Gln Arg Phe Arg Gln Lys Ser Lys Ala Ser Phe Leu Leu Leu Ala Ser  
60 65 70

ggc ctg gta atc act gat ttc ttt ggc cat ctc atc aat gga gcc ata 412  
Gly Leu Val Ile Thr Asp Phe Phe Gly His Leu Ile Asn Gly Ala Ile  
75 80 85

gca gta ttt gta tat gct tct gat aaa gaa tgg atc cgc ttt gac caa 460  
Ala Val Phe Val Tyr Ala Ser Asp Lys Glu Trp Ile Arg Phe Asp Gln  
90 95 100

tca aat gtc ctt tgc agt att ttt ggt atc tgc atg gtg ttt tct ggt 508  
Ser Asn Val Leu Cys Ser Ile Phe Gly Ile Cys Met Val Phe Ser Gly  
105 110 115

ctg tgc cca ctt ctt cta ggc agt gtg atg gcc att gag cgg tgt att 556  
Leu Cys Pro Leu Leu Gly Ser Val Met Ala Ile Glu Arg Cys Ile  
120 125 130 135

gga gtc aca aaa cca ata ttt cat tct acg aaa att aca tcc aaa cat 604  
Gly Val Thr Lys Pro Ile Phe His Ser Thr Lys Ile Thr Ser Lys His  
140 145 150

gtg aaa atg atg tta agt ggt gtg tgc ttg ttt gct gtt ttc ata gct 652  
Val Lys Met Met Leu Ser Gly Val Cys Leu Phe Ala Val Phe Ile Ala  
155 160 165

ttg ctg ccc atc ctt gga cat cga gac tat aaa att cag gcg tcg agg 700  
Leu Leu Pro Ile Leu Gly His Arg Asp Tyr Lys Ile Gln Ala Ser Arg  
170 175 180

acc tgg tgt ttc tac aac aca gaa gac atc aaa gac tgg gaa gat aga 748  
Thr Trp Cys Phe Tyr Asn Thr Glu Asp Ile Lys Asp Trp Glu Asp Arg  
185 190 195

ttt tat ctt cta ctt ttt tct ttt ctg ggg ctc tta gcc ctt ggt gtt 796  
Phe Tyr Leu Leu Leu Phe Ser Phe Leu Gly Leu Leu Ala Leu Gly Val  
200 205 210 215

tca ttg ttg tgc aat gca atc aca gga att aca ctt tta aga gtt aaa 844  
Ser Leu Leu Cys Asn Ala Ile Thr Gly Ile Thr Leu Leu Arg Val Lys  
220 225 230

ttt aaa agt cag cag cac aga caa ggc aga tct cat cat ttg gaa atg 892  
Phe Lys Ser Gln Gln His Arg Gln Gly Arg Ser His His Leu Glu Met

235	240	245	
gta atc cag ctc ctg gcg ata atg tgt gtc tcc tgt att tgt tgg agc			940
Val Ile Gln Leu Leu Ala Ile Met Cys Val Ser Cys Ile Cys Trp Ser			
250	255	260	
cca ttt ctg gtt aca atg gcc aac att gga ata aat gga aat cat tct			988
Pro Phe Leu Val Thr Met Ala Asn Ile Gly Ile Asn Gly Asn His Ser			
265	270	275	
ctg gaa acc tgt gaa aca aca ctt ttt gct ctc cga atg gca aca tgg			1036
Leu Glu Thr Cys Glu Thr Thr Leu Phe Ala Leu Arg Met Ala Thr Trp			
280	285	290	295
aat caa atc tta gat cct tgg gta tat att ctt cta cga aag gct gtc			1084
Asn Gln Ile Leu Asp Pro Trp Val Tyr Ile Leu Leu Arg Lys Ala Val			
300	305	310	
ctt aag aat ctc tat aag ctt gcc agt caa tgc tgt gga gtg cat gtc			1132
Leu Lys Asn Leu Tyr Lys Leu Ala Ser Gln Cys Cys Gly Val His Val			
315	320	325	
atc agc tta cat att tgg gag ctt agt tcc att aaa aat tcc tta aag			1180
Ile Ser Leu His Ile Trp Glu Leu Ser Ser Ile Lys Asn Ser Leu Lys			
330	335	340	
gtt gct gct att tct gag tca cca gtt gca gag aaa tca gca agc acc			1228
Val Ala Ala Ile Ser Glu Ser Pro Val Ala Glu Lys Ser Ala Ser Thr			
345	350	355	
tagcttaata ggacagtaaa tctgtgtggg gctagaacaa aaattaagac atgtttggca			1288
atatttcagt tagttaata cctgttagcct aactggaaaa ttcaggcttc atcatgtagt			1348
ttgaagatac tattgtcaga ttcaagggttt gaaatttgc aaataaacag gataactgta			1408
cattttcaac ttgttttgc caatgggagg tagacacaat aaaataatgc catgggagtc			1468
acactgaaag caattttgag cttatctgca ttatttatgc tttagtgc aaatctgttg			1528
aggtctaattg cctctacttg gcctatttgc cagagaacat cttatgcag cctgcatagt			1588
gaaatggta tttttagatc accgctctgt agctaaccct tataaactag gctcagtaaa			1648
ataaaagcact cttattttt gatctggcct attttgccttc tcattgtgta gcctcaatta			1708
acacatgcat ggtcatgaca cccagaattc atgatggttt gttataacaa cctctgcata			1768
ttccaggtct ggcagacagg ttgcctgacc ctgcaatcct atctagaatg ggcccattct			1828
tgtcacattt gacaaatagg actgcctaca tttatttata tgaaggtcga ttgttgg			1888
aagtgtttt tcatgtcata gatttagcaat ttcaaaataa ttatttttc tctgaaaatt			1948
ttgtgtgtca ttgcacaata aataattttt agagaaacaa aggcttttc tcagcacatt			2008
gatggcaac tagaattaca gcagttcaa actctaccat ggataatgca aacaaaccga			2068
agctacatgc caatgatagg tgcaaagaat attggcaaaa ggtgctttac cttgagccat			2128
tatttgtc agagaacaaa agaaacagaa tcaatataa aattcaaaaga cttatctgcag			2188
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aggttcatta aatttgcattt atggcatatt ctaaaggctg tgctaccagt actaagaggg			2308
gaagactggc aatttgccaa gcactgggg attattataa caattaacta ggagatcaag			2368
agataataat ctctccccaa attttccaaat aataatttgcg actttttctt tgcttgg			2428
tgttaattcaa cccaaagaat tcaatacc attcaaatttgcct taggtct atcagaaatt			2488
agggaaaggtt gtcctgctt ataataggaa aatgtatttc tgtataagat ttcttgctt			2548
tcattaaaaa tgggattcat taaaaattt atctttccct gttaggctga ttccagattc			2608

tcttagggaaat ctgggtgaagt aaccagaaga ctttcagatg gtttatttgc tttcagcaga 2668  
gaattttattt catacagttt cttaaagatgt ttgatgtctt gtgaacagag atataaggaa 2728  
ccattctcca tccttcctta tcatgctggg tacaatgctt ctatgaatat ttccatgtat 2788  
tttgactggg gagaggcatg gagaagaaac tctcattca gggctccagg atccttctcc 2848  
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tgtgtactga cttgaggaga tcttgcacaca tggccatgtg caaggctta aggagtgaga 2968  
gagatgtgtatc catatcttag gagggttatac tatgttatct gagtatatgt ttgggttaacc 3028  
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aaaaaaaaa 3095

<210> 14  
<211> 359  
<212> PRT  
<213> *Homo sapiens*

<400> 14  
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 Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
 35 40 45  
 Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
 50 55 60  
 Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
 65 70 75 80  
 His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
 85 90 95  
 Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
 100 105 110  
 Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val  
 115 120 125  
 Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
 130 135 140  
 Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
 145 150 155 160  
 Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp  
 165 170 175  
 Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp  
 180 185 190  
 Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu  
 195 200 205  
 Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly  
 210 215 220  
 Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
 225 230 235 240  
 Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys  
 245 250 255  
 Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Val Thr Met Ala Asn Ile  
 260 265 270  
 Gly Ile Asn Gly Asn His Ser Leu Glu Thr Cys Glu Thr Thr Leu Phe  
 275 280 285  
 Ala Leu Arg Met Ala Thr Trp Asn Gln Ile Leu Asp Pro Trp Val Tyr

290	295	300
Ile Leu Leu Arg Lys Ala Val Leu Lys Asn Leu Tyr Lys Leu Ala Ser		
305	310	315
Gln Cys Cys Gly Val His Val Ile Ser Leu His Ile Trp Glu Leu Ser		320
325	330	335
Ser Ile Lys Asn Ser Leu Lys Val Ala Ala Ile Ser Glu Ser Pro Val		
340	345	350
Ala Glu Lys Ser Ala Ser Thr		
355		

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<211> 9		
<212> PRT		
<213> Homo sapiens		
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Ser Pro Phe Leu Gly Tyr Arg Ile Ile		
1	5	
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<400> 18		
Ser Pro Phe Leu Lys Ile Glu Gly Lys		
1	5	

<210> 19  
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1 5

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<212> PRT  
<213> Homo sapiens

<400> 20  
Ser Pro Phe Leu Thr His Trp Gly Lys  
1 5

<210> 21  
<211> 31  
<212> PRT  
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